

10/542769

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SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Förderung der Wissensc

<120> L-amino acid oxidase with cytotoxic activity from
Aplysia punctata

<130> 29644PWO_2

<140> PCT/EP04/00423

<141> 2004-01-20

<150> EP03001232.2

<151> 2003-01-20

<150> EP03026613.4

<151> 2003-11-19

<160> 72

<170> PatentIn Ver. 2.1

<210> 1

<211> 1608

<212> DNA

<213> Aplysia punctata

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<222> (1)..(1608)

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His Ala Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val
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tgc ggt tct acc tac gat gtg gcc gtc gtg ggg ggc ggg cct ggg gga 144
Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
35 40 45

gct aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg 192
Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
50 55 60

ttc gag tac tcg gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg 240
Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
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ccc aac aca ccc gac gtt aac ctg gag att ggc ggc atg agg ttc atc 288
Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
85 90 95

gaa ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta 336

Glu	Gly	Ala	Met	His	Arg	Leu	Trp	Arg	Val	Ile	Ser	Glu	Leu	Gly	Leu			
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Thr	Pro	Lys	Val	Phe	Lys	Glu	Gly	Phe	Gly	Lys	Glu	Gly	Arg	Gln	Arg			
115																125		
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Phe	Tyr	Leu	Arg	Gly	Gln	Ser	Leu	Thr	Lys	Lys	Gln	Val	Lys	Ser	Gly			
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gac	gta	ccc	tat	gac	ctc	agc	ccg	gag	gag	aaa	gaa	aac	cag	gga	aat		480	
Asp	Val	Pro	Tyr	Asp	Leu	Ser	Pro	Glu	Glu	Lys	Glu	Asn	Gln	Gly	Asn			
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ctg	gtc	gaa	tac	tac	ctg	gag	aaa	ctg	aca	ggt	cta	caa	ctc	aac	ggc		528	
Leu	Val	Glu	Tyr	Tyr	Leu	Glu	Lys	Leu	Thr	Gly	Leu	Gln	Leu	Asn	Gly			
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gag	ccg	ctc	aaa	cgt	gag	gtt	gcg	ctt	aaa	cta	acc	gtg	ccg	gac	ggc		576	
Glu	Pro	Leu	Lys	Arg	Glu	Val	Ala	Leu	Lys	Leu	Thr	Val	Pro	Asp	Gly			
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Arg	Phe	Leu	Tyr	Asp	Leu	Ser	Phe	Asp	Glu	Ala	Met	Asp	Leu	Val	Ala			
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tcc	cct	gag	ggc	aaa	gag	ttc	acc	cga	gac	acg	cac	gtc	ttc	aca	gga		672	
Ser	Pro	Glu	Gly	Lys	Glu	Phe	Thr	Arg	Asp	Thr	His	Val	Phe	Thr	Gly			
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Glu	Val	Thr	Leu	Asp	Ala	Ser	Ala	Val	Ser	Leu	Phe	Asp	Asp	His	Leu			
225																235	240	
gga	gag	gac	tac	tat	ggc	agt	gag	atc	tac	acc	cta	aag	gaa	gga	ctg		768	
Gly	Glu	Asp	Tyr	Tyr	Gly	Ser	Glu	Ile	Tyr	Thr	Leu	Lys	Glu	Gly	Leu			
245																250	255	
tct	tcc	gtc	cca	caa	ggg	ctc	cta	cag	gct	ttt	ctg	gac	gcc	gca	gac		816	
Ser	Ser	Val	Pro	Gln	Gly	Leu	Leu	Gln	Ala	Phe	Leu	Asp	Ala	Ala	Asp			
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Ser	Asn	Glu	Phe	Tyr	Pro	Asn	Ser	His	Leu	Lys	Ala	Leu	Arg	Arg	Lys			
275																280	285	
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Thr	Asn	Gly	Gln	Tyr	Val	Leu	Tyr	Phe	Glu	Pro	Thr	Thr	Ser	Lys	Asp			
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gga	caa	acc	aca	atc	aac	tat	ctg	gaa	ccc	ctg	cag	gtt	gtg	tgt	gca		960	
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caa	aga	gtc	atc	ctg	gcc	atg	ccg	gta	tac	gct	ctg	aac	caa	cta	gac		1008	
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325	330	335	
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cgc ccg att cct gca agt aag gtg ttc atg tcc ttt gat cag ccc tgg Arg Pro Ile Pro Ala Ser Lys Val Phe Met Ser Phe Asp Gln Pro Trp 355	360	365	1104
tgg ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu 370	375	380	1152
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gag gct tat ggc gtg gag cga gac tcg atc ccg gaa ccc gtg acc gcc Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala 450	455	460	1392
gct tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr 465	470	475	1440
tgg agg gcc ggc ttc cat ttc gat gac gtc atc age acc atg cgt cgc Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg 485	490	495	1488
ccg tca ctg aaa gat gag gta tac gtg gtg gga gcc gac tac tcc tgg Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp 500	505	510	1536
gga ctt atc tcc tcc tgg ata gag ggc qct ctg gag acc tcg gaa aac Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn 515	520	525	1584
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Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
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Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
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Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu
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145 150 155 160

Leu Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly
165 170 175

Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
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Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
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Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
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Gln Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp		
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Trp Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val		
340	345	350
Arg Pro Ile Pro Ala Ser Lys Val Phe Met Ser Phe Asp Gln Pro Trp		
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Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu		
370	375	380
Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr		
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Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg		
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Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr		
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Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr		
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Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala		
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Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg		
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Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp		
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Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn		
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Val Ile Asn Asp Tyr Phe Leu		
530	535	

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Ala Asp Gly Val Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys
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ggc tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga gct 144
Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
35 40 45

aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc 192
Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
50 55 60

gag tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc 240
Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
65 70 75 80

aac aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag 288
Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
85 90 95

ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc 336
Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
100 105 110

ccc aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt 384
Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
115 120 125

tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac 432
Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
130 135 140

gta ccc tat gac ctc agc ccg qag gag aaa gaa aac cag gga aat ctg 480
Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gin Gly Asn Leu
145 150 155 160

gtc gaa tac tac ctg gag aaa ctg aca ggt cta caa ctc aat ggt gaa 528
Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly Glu
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gtc acc ctg ggc gcg tcg gct gtc tcc ctc ttc gac gac cac ctg gga Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly 225	230	235	720
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tcc gtc cct caa ggg ctc cta cag gct ttt ctg gac gcc gca gac tcc Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser 260	265	270	816
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caa acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca cag Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln 305	310	315	960
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aat cag ctc aag aat gac cga gcc acc caa gcg tac gct gcc gtg cgc Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg 340	345	350	1056
ccg att cct gca agt aag gtg ttc atg acc ttt gat cag ccc tgg tgg Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp 355	360	365	1104
ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe 370	375	380	1152
agt caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile 385	390	395	1200
ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu			1248

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ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn 420	425	430	1296
cag gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu 435	440	445	1344
gcc tat ggc gtg gag cga gac tcg atc cgg gaa ccc gtg acc gcc gct Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala 450	455	460	1392
tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc tgg Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp 465	470	475	1440
agg gcc ggc ttc cat ttc gat gac gtc atc agc acc atg cgt cgc ccg Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro 485	490	495	1488
tca ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly 500	505	510	1536
ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tca gaa aac gtc Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val 515	520	525	1584
atc aac gac tac ttc ctc taa Ile Asn Asp Tyr Phe Leu 530	535		1605
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Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro 65	70	75	80
Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu			

85

90

95

Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
100 105 110

Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
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Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
130 135 140

Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu
145 150 155 160

Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly Glu
165 170 175

Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg
180 185 190

Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser
195 200 205

Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu
210 215 220

Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly
225 230 235 240

Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser
245 250 255

Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser
260 265 270

Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr
275 280 285

Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly
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Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln
305 310 315 320

Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp
325 330 335

Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg
340 345 350

Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp
355 360 365

Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe
370 375 380

Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile
 385 390 395 400
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 420 425 430
 Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu
 435 440 445
 Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala
 450 455 460
 Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp
 465 470 475 480
 Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro
 485 490 495
 Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly
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 Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
 35 40 45

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 Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln. Leu Pro Asn
 50 55 60

aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag ggc 240
 Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
 65 70 75 80

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 Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro
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 Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr
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 145 150 155 160

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 165 170 175

 ctc tat gac ctc tcg ttt gac gaa gcc atg gac ctg gtt gcc tcc cct 576
 Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro
 180 185 190

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 Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val
 195 200 205

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 Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu
 210 215 220

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 Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser
 225 230 235 240

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 Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn
 245 250 255

 gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag acc aac 816
 Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn
 260 265 270

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 Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln
 275 280 285

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Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg		
290	295	300
gtc atc ctg gcc atg ccg gtc tac gct ctc aac caa ctg gac tgg aat		960
Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn		
305	310	315
320		
cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc ccg		1008
Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro		
325	330	335
att cct gca agt aaa gtg ttc atg acc ttt gat cag ccc tgg tgg ttg		1056
Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu		
340	345	350
gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc agc		1104
Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser		
355	360	365
caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc ctg		1152
Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu		
370	375	380
atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag ctg		1200
Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu		
385	390	395
400		
aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac cag		1248
Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln		
405	410	415
gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag gct		1296
Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala		
420	425	430
435		
tat ggc gtg gaa cga gac tcg atc ccg gaa ccc gtc acc gcc gct tcc		1344
Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser		
440	445	
450		
cag ttc tgg acc gac tac ccg ttc ggc tgt gga tgg atc acc tgg agg		1392
Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg		
455	460	
465		
gca ggc ttc cat ttt gat gac gtc atc agc acc atg cgt cgc ccg tca		1440
Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser		
470	475	480
485		
ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga cit		1488
Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu		
490	495	
495		
atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac gtc atc		1536
Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile		
500	505	510
510		
aac gac tac ttc ctc taa		1554

Asn Asp Tyr Phe Leu
515

<210> 6
<211> 517
<212> PRT
<213> Aplysia punctata

<400> 6
Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys Gly
1 5 10 15

Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
20 25 30

Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
35 40 45

Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
50 55 60

Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
65 70 75 80

Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro
85 90 95

Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr
100 105 110

Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val
115 120 125

Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val
130 135 140

Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro
145 150 155 160

Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe
165 170 175

Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro
180 185 190

Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val
195 200 205

Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu
210 215 220

Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser
225 230 235 240

Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn
245 250 255

Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn
260 265 270

Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln
275 280 285

Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg
290 295 300

Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn
305 310 315 320

Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro
325 330 335

Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
340 345 350

Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser
355 360 365

Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu
370 375 380

Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu
385 390 395 400

Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln
405 410 415

Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala
420 425 430

Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser
435 440 445

Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg
450 455 460

Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser
465 470 475 480

Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu
485 490 495

Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile
500 505 510

Asn Asp Tyr Phe Leu
515

<210> 7
<211> 600
<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(600)

<400> 7

atg tct tca gga aat gct aaa att ggg cac cct gcc ccc aac ttc aaa 48
Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
1 5 10 15

gcc aca gct gtt atg cca gat ggt cag ttt aaa gat atc agc ctg tct 96
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
20 25 30

gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt gac ttc 144
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Tyr Pro Leu Asp Phe
35 40 45

acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg gca gaa 192
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
50 55 60

gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg gat tct 240
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65 70 75 80

cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa gga gga 288
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly
85 90 95

ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc acc att 336
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
100 105 110

gct cag gat tat ggg gtc tta aag gct gat gaa ggc atc tcg ttc agg 384
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
115 120 125

ggc ctt ttt atc att gat gat aag ggt att ctt ccg cag atc act gta 432
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
130 135 140

aat gac ctc cct gtt ggc cgc tct gtg gat gag act ttg aga cta gtt 480
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145 150 155 160

cag gcc ttc cag ttc act gac aaa cat ggg gaa gtg tgc cca gct ggc 528
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
165 170 175

tgg aaa cct ggc agt gat acc atc aag cct gat gtc caa aag agc aaa 576
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
180 185 190

gaa tat ttc tcc aag cag aag tga 600
Glu Tyr Phe Ser Lys Gln Lys

195

200

<210> 8
<211> 199
<212> PRT
<213> Human

<400> 8
Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
1 5 10 15
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
20 25 30
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Tyr Pro Leu Asp Phe
35 40 45
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
50 55 60
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65 70 75 80
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
85 90 95
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
100 105 110
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
115 120 125
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
130 135 140
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145 150 155 160
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
165 170 175
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
180 185 190
Glu Tyr Phe Ser Lys Gln Lys
195

<210> 9
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

double-stranded RNA molecule

<400> 9
ggcugaugaa ggcaucucg 19

<210> 10
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 10
augcuaaaaau ugggcaccc 19

<210> 11
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 11
ugcuaaaaauu qggcacccu 19

<210> 12
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 12
cuucaaagcc acagcuguu 19

<210> 13
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 13
agccacagcu guuaugcca 19

<210> 14
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 14
gccacagcug uuaugccag 19

<210> 15
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 15
agauaucagc cugucugac 19

<210> 16
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 16
gauaucagcc ugucugacu 19

<210> 17
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 17
gaaacucaac ugccaagug 19

<210> 18
<211> 19
<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 18
acucaacugc caagugauu 19

<210> 19
<211> 19
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 19
cuacaacugcc aagugauug 19

<210> 20
<211> 19
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 20
cugccaagug auuggugcu 19

<210> 21
<211> 19
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 21
gugauuggug cuucugugg 19

<210> 22
<211> 19
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 22
gaaacaagga ggacuggga 19

<210> 23
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 23
cauuccuuug guaucagac 19

<210> 24
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 24
aggcugauga aggcaucuc 19

<210> 25
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 25
gcgcaccáuu gcucaggau 19

<210> 26
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 26
ggguauucuu cggcagauc 19

<210> 27
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 27
accuggcagu gauaccauc 19

<210> 28
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 28
ccuggcagug auaccauc 19

"

<210> 29
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 29
gccugauguc caaaagagc 19

<210> 30
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic double-stranded RNA molecule

<400> 30
cuggacuucc agaagaaca 19

<210> 31
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 31
cuaacgcuga guacuucga

19

<210> 32
<211> 7
<212> PRT
<213> Aplysia

<400> 32
Asp Gly Glu Asp Ala Ala Val
1 5

<210> 33
<211> 9
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)
<223> Asp can be Asp or Gln

<220>
<221> MOD_RES
<222> (3)
<223> Ile can be Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Gln can be Gln or Arg

<220>
<221> MOD_RES
<222> (9)
<223> Pro can be Pro or Gln

<400> 33
Asp Gly Ile Cys Arg Asn Gln Arg Pro
i 5

<210> 34
<211> 4
<212> PRT
<213> Aplysia

<400> 34

Phe Ala Asp Ser
1

<210> 35
<211> 8
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (5)
<223> Ile can be Ile or Leu

<400> 35
Gly Pro Asp Gly Ile Val Ala Asp
1 5

<210> 36
<211> 7
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (6)
<223> Lys can be Lys or Gln

<220>
<221> MOD_RES
<222> (7)
<223> Ile can be Ile or Leu

<400> 36
Pro Gly Glu Val Ser Lys Ile
1 5

<210> 37
<211> 15
<212> PRT
<213> Aplysia

<400> 37
Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro Ile Pro Ala Ser Lys
1 5 10 15

<210> 38
<211> 13
<212> PRT
<213> Aplysia

<400> 38
Asp Ser Gly Leu Asp Ile Ala Val Glu Tyr Ser Asp Arg
1 5 10

<210> 39
<211> 12
<212> PRT
<213> Aplysia

<400> 39
Gly Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys
1 5 10

<210> 40
<211> 442
<212> DNA
<213> Aplysia

<400> 40
caagacgggg aagacaagga gtttgcggga gaaatcgta gcgtcagagt gctgaaggcg 60
ttcggcaagc ctggctacgg ttacaagca g cccctcggtca aggaaggcaa ggactacgtg 120
agcagcggca gcgttcttca cgtgctgcag tgcgcggct tcttcgaggt gtgcgtacgag 180
gagaggatca ccaccacgccc agccacgact gtcgcgtcag cagaggtaca atgaaaaaag 240
ttcatcgcaa cccacaaaatt ggaggagact gttgatggaa ggatcgta catcgagctt 300
gtccagagac tgaagaaaaata atccggataac ggtccaagtq gcgggtctgg ttatggcaac 360
ggcatggtc aaagacccgg ttacggatac gggtctggta gtggaaagtgg ctaccccccc 420
agaggaggat acaacccaaa ag 442

<210> 41
<211> 147
<212> PRT
<213> Aplysia

<400> 41
Gln Asp Gly Glu Asp Lys Glu Phe Asp Gly Glu Ile Val Ser Val Arg
1 5 10 15

Val Leu Lys Ala Phe Gly Lys Pro Gly Tyr Gly Tyr Lys Gln Pro Ser
20 25 30

Cys Lys Glu Gly Lys Asp Tyr Val Ser Ser Gly Ser Val Leu His Val
35 40 45

Leu Gln Cys Ala Gly Phe Phe Glu Val Cys Tyr Glu Glu Arg Ile Thr
50 55 60

Thr Gln Pro Ala Thr Thr Val Ala Ala Ala Glu Val Gln Cys Lys Lys
65 70 75 80

Phe Ile Ala Thr His Lys Leu Glu Glu Thr Val Asp Gly Arg Ile Val
85 90 95

Ser Ile Glu Leu Val Gln Arg Leu Lys Lys Gln Ser Gly Tyr Gly Pro
100 105 110

Ser Gly Gly Ser Gly Tyr Gly Asn Gly His Gly Gln Arg Pro Gly Tyr
115 120 125

Gly Tyr Gly Ser Gly Ser Gly Tyr Ala Pro Arg Gly Gly Tyr
130 135 140

Asn Pro Lys
145

<210> 42

<211> 462

<212> DNA

<213> Aplysia

<400> 42

taccggccccc gccaccactn tngcaccaggc agaaccaacc tgcgagaagc tgtccgtntg 60
gttcaacgtg ganaagaaat tcgaagggtc cagaatcggt agtttcaagc tcatccgcct 120
gttcaacagg tncaagaagt gcaagaaagn ccagtattcc gtgtctggcg atgatgagga 180
cncattcggtt gtcagtggtt gttctggcggt gttccaggtt tgctacgaag aacaaacggc 240
gcccgctaca accnccacag aagccccgaa gccagagcca agaagaccca agagaaaaaa 300
tttcccaatc aaattntgta aacactgatg ggttaatntg acgaccagtg cgtctgcgaa 360
agaatcatgt tatggttcat gatgtcatgc tcttaatata ggtttaacg 420
tacagacatt aaaactcatt gttcaaaaaaaaaaa aa 462

<210> 43

<211> 155

<212> PRT

<213> Aplysia

<220>

<221> MOD_RES

<222> (1)..(155)

<223> Xaa = unknown amino acid or STOP-codon

<400> 43

Tyr Arg Pro Arg His His Xaa Xaa Thr Ser Arg Thr Asn Leu Arg Glu
1 5 10 15

Ala Val Arg Xaa Val Gln Arg Gly Xaa Glu Ile Arg Arg Phe Gln Asn
20 25 30

Arg Glu Phe Gln Ala His Pro Pro Val Gln Gln Xaa Gln Glu Val Gln
35 40 45

Glu Xaa Pro Val Phe Arg Val Trp Arg Xaa Xaa Gly Xaa Ile Arg Cys
50 55 60

Gln Trp Leu Phe Trp Arg Val Pro Gly Xaa Leu Arg Arg Thr Asn Gly
65 70 75 80

Ala	Arg	Tyr	Asn	Xaa	His	Arg	Ser	Pro	Glu	Ala	Arg	Ala	Lys	Lys	Thr
					85				90					95	
Gln	Glu	Glu	Lys	Phe	Pro	Asn	Gln	Ile	Xaa	Xaa	Thr	Leu	Met	Gly	Xaa
					100				105					110	
Xaa	Asp	Asp	Gln	Cys	Val	Cys	Glu	Arg	Ile	Met	Leu	Trp	Phe	Met	Met
					115				120					125	
Ser	Cys	Ser	Xaa	Xaa	Tyr	Arg	Leu	Xaa	Arg	Leu	Thr	Arg	Tyr	Arg	His
					130				135					140	
Xaa	Asn	Ser	Leu	Phe	Lys	Lys	Lys	Lys	Lys	Lys					
					145				150					155	

<210> 44
<211> 153
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(153)
<223> Xaa = unknown amino acid or STOP-codon

<400> 44
Thr Ala Pro Ala Thr Thr Xaa Ala Pro Ala Glu Pro Thr Cys Glu Lys
1 5 10 15

Leu Ser Xaa Trp Phe Asn Val Xaa Lys Lys Phe Glu Gly Ser Arg Ile
20 25 30

Val Ser Phe Lys Leu Ile Arg Leu Phe Asn Arg Xaa Lys Lys Cys Lys
35 40 45

Lys Xaa Gln Tyr Ser Val Ser Gly Asp Asp Glu Asp Xaa Phe Val Val
50 55 60

Ser Gly Cys Ser Gly Val Phe Gln Xaa Cys Tyr Glu Glu Gln Thr Ala
65 70 75 80

Pro Ala Thr Thr Xaa Thr Glu Ala Pro Lys Pro Glu Pro Arg Arg Pro
85 90 95

Lys Arg Lys Asn Phe Pro Ile Lys Phe Xaa Lys His Xaa Trp Val Asn
100 105 110

Xaa Thr Thr Ser Ala Ser Ala Lys Glu Ser Cys Tyr Gly Ser Xaa Cys
115 120 125

His Ala Leu Asn Ile Gly Cys Asn Val Xaa Arg Asp Thr Asp Ile Lys
130 135 140

Thr His Cys Ser Lys Lys Lys Lys
145 150

<210> 46
<211> 9
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (3)
<223> Ile can be Ile or Val

<400> 46

Asp Gly Ile Cys Arg Asn Arg Arg Gln
1 5

<210> 47
<211> 14
<212> PRT
<213> Aplysia

<400> 47
Asp Ser Gly Leu Asp Ile Ala Val Phe Glu Tyr Ser Asp Arg
1 5 10

<210> 48

<211> 7
<212> PRT
<213> Aplysia

<400> 48
Val Phe Glu Tyr Ser Asp Arg
1 5

<210> 49
<211> 16
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid, in particular Thr

<400> 49
Leu Phe Xaa Tyr Gln Leu Pro Asn Thr Pro Asp Val Asn Leu Glu Ile
1 5 10 15

<210> 50
<211> 10
<212> PRT
<213> Aplysia

<400> 50
Val Ile Ser Glu Leu Gly Leu Thr Pro Lys
1 5 10

<210> 51
<211> 11

<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = any amino acid, in particular Met

<400> 51
Val Ile Leu Ala Xaa Pro Val Tyr Ala Leu Asn
1 5 10

<210> 52
<211> 8
<212> PRT
<213> Aplysia

<400> 52
Val Phe Met Thr Phe Asp Gln Pro
1 5

<210> 53
<211> 10
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (6)
<223> Phe can be Phe or Ser

<400> 53
Ser Asp Ala Leu Phe Phe Gln Met Tyr Asp
1 5 10

<210> 54
<211> 18
<212> PRT
<213> Aplysia

<400> 54
Ser Glu Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly
1 5 10 15

Leu Lys

<210> 55

<211> 21
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (12)
<223> Gln can be Gln or Gly

<400> 55
Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gln Tyr Asn Gln Val
1 5 10 15

Thr Glu Pro Leu Lys
20

<210> 56
<211> 28
<212> PRT
<213> Aplysia

<400> 56
Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn Ser Ala Tyr Met
1 5 10 15

Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
20 25

<210> 57
<211> 8
<212> PRT
<213> Aplysia

<400> 57
Arg Val Gly Gly Arg Leu Phe Thr
1 5

<210> 58
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
tccttaacgt a ggtctagacc ttttgcatttt tttttt 45

<210> 59

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<223> n = i

<400> 59
tcgtgttcga rtactcngay cg 22

<210> 60
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 60
ctgttaggtct agacctgttg ca 22

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 61
ccgtgtagat ctcactgcc ta 22

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 62
ccgttgagtt gtagacct 18

<210> 63
<211> 36
<212> DNA

<213> Artificial Sequence
<220>
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<220>
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<400> 72
gacttgcct tcgagtgacc gta

23